

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/080,354ADATE: 02/01/94  
TIME: 18:38:47

INPUT SET: S7245.raw

## SEQUENCE LISTING

## (1) General Information:

- (i) APPLICANT: Breece, Tim  
Hayenga, Kirk  
Rinderknecht, Ernst  
Vandlen, Richard  
Yansura, Daniel

error on p. 17 →

(ii) TITLE OF INVENTION: PROCESS FOR PRODUCING RELAXIN

(iii) NUMBER OF SEQUENCES: 40

## (iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Mr. Walter H. Dreger  
(B) STREET: 4 Embarcadero Center, Suite 3400  
(C) CITY: San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94111

## (v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

## (vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/080,354  
(B) FILING DATE: 21-JUN-1993  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Dreger, Walter H.  
(B) REGISTRATION NUMBER: 24,190  
(C) REFERENCE/DOCKET NUMBER: A-58117/WH

## (ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (415) 781-1989  
(B) TELEFAX: (415) 398-3249

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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52 (ii) MOLECULE TYPE: peptide

53

54 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

55

56 Met Lys Lys Asn Ile Ala Phe Leu Leu Lys Arg

57

1

5

10

58

59

60 (2) INFORMATION FOR SEQ ID NO:2:

61

62 (i) SEQUENCE CHARACTERISTICS:

63 (A) LENGTH: 29 amino acids

64 (B) TYPE: amino acid

65 (C) STRANDEDNESS: single

66 (D) TOPOLOGY: linear

67

68 (ii) MOLECULE TYPE: peptide

69

70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

71

72 Asp Ser Trp Met Glu Glu Val Ile Lys Leu Cys Gly Arg Glu Leu Val

73

1

5

10

15

74

75 Arg Ala Gln Ile Ala Ile Cys Gly Met Ser Thr Trp Ser

76

20

25

77

78

79 (2) INFORMATION FOR SEQ ID NO:3:

80

81 (i) SEQUENCE CHARACTERISTICS:

82 (A) LENGTH: 13 amino acids

83 (B) TYPE: amino acid

84 (C) STRANDEDNESS: single

85 (D) TOPOLOGY: linear

86

87 (ii) MOLECULE TYPE: peptide

88

89 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

90

91 Lys Arg Lys Pro Thr Gly Tyr Gly Ser Arg Lys Lys Arg

92

1

5

10

93

94

95 (2) INFORMATION FOR SEQ ID NO:4:

96

97 (i) SEQUENCE CHARACTERISTICS:

98 (A) LENGTH: 24 amino acids

99 (B) TYPE: amino acid

100 (C) STRANDEDNESS: single

101 (D) TOPOLOGY: linear

102

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103 (ii) MOLECULE TYPE: peptide  
104  
105 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
106  
107 Gln Leu Tyr Ser Ala Leu Ala Asn Lys Cys Cys His Val Gly Cys Thr  
108 1 5 10 15  
109  
110 Lys Arg Ser Leu Ala Arg Phe Cys  
111 20  
112  
113  
114 (2) INFORMATION FOR SEQ ID NO:5:  
115  
116 (i) SEQUENCE CHARACTERISTICS:  
117 (A) LENGTH: 13 amino acids  
118 (B) TYPE: amino acid  
119 (C) STRANDEDNESS: single  
120 (D) TOPOLOGY: linear  
121  
122 (ii) MOLECULE TYPE: peptide  
123  
124 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
125  
126 Lys Arg Lys Pro Thr Gly Tyr Gly Ser Arg Lys Lys Arg  
127 1 5 10  
128  
129  
130 (2) INFORMATION FOR SEQ ID NO:6:  
131  
132 (i) SEQUENCE CHARACTERISTICS:  
133 (A) LENGTH: 13 amino acids  
134 (B) TYPE: amino acid  
135 (C) STRANDEDNESS: single  
136 (D) TOPOLOGY: linear  
137  
138 (ii) MOLECULE TYPE: peptide  
139  
140 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  
141  
142 Asp Lys Lys Arg Thr Gly Tyr Gly Ser Arg Arg Arg Lys  
143 1 5 10  
144  
145  
146 (2) INFORMATION FOR SEQ ID NO:7:  
147  
148 (i) SEQUENCE CHARACTERISTICS:  
149 (A) LENGTH: 13 amino acids  
150 (B) TYPE: amino acid  
151 (C) STRANDEDNESS: single  
152 (D) TOPOLOGY: linear  
153

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/080,354A

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154      (ii) MOLECULE TYPE: peptide
155
156      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
157
158      Asp Lys Lys Arg Thr Gly Tyr Gly Ser Arg Lys Lys Arg
159          1             5             10
160
161
162      (2) INFORMATION FOR SEQ ID NO:8:
163
164          (i) SEQUENCE CHARACTERISTICS:
165              (A) LENGTH: 13 amino acids
166              (B) TYPE: amino acid
167              (C) STRANDEDNESS: single
168              (D) TOPOLOGY: linear
169
170          (ii) MOLECULE TYPE: peptide
171
172          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
173
174          Lys Arg Lys Pro Thr Gly Tyr Gly Ser Arg Arg Arg Lys
175              1             5             10
176
177
178      (2) INFORMATION FOR SEQ ID NO:9:
179
180          (i) SEQUENCE CHARACTERISTICS:
181              (A) LENGTH: 231 base pairs
182              (B) TYPE: nucleic acid
183              (C) STRANDEDNESS: single
184              (D) TOPOLOGY: linear
185
186          (ii) MOLECULE TYPE: cDNA
187
188          (ix) FEATURE:
189              (A) NAME/KEY: CDS
190              (B) LOCATION: 1..231
191
192          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
193
194      ATG AAA AAG AAT ATC GCA TTT CTT CTT AAA CGG GAC TCA TGG ATG GAG      48
195      Met Lys Lys Asn Ile Ala Phe Leu Leu Lys Arg Asp Ser Trp Met Glu
196          1             5             10             15
197
198      GAA GTT ATT AAA TTA TGC GGC CGC GAA TTA GTT CGC GCG CAG ATT GCC      96
199      Glu Val Ile Lys Leu Cys Gly Arg Glu Leu Val Arg Ala Gln Ile Ala
200              20             25             30
201
202      ATT TGC GGC ATG AGC ACC TGG AGC AAA AGG AAA CCC ACT GGT TAT GGT      144
203      Ile Cys Gly Met Ser Thr Trp Ser Lys Arg Lys Pro Thr Gly Tyr Gly
204          35             40             45

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205  
206 TCT CGA AAA AAG AGA CAA CTC TAC AGT GCA TTG GCT AAT AAA TGT TGC 192  
207 Ser Arg Lys Lys Arg Gln Leu Tyr Ser Ala Leu Ala Asn Lys Cys Cys  
208 50 55 60  
209  
210 CAT GTT GGT TGT ACC AAA AGA TCT CTT GCT AGA TTT TGC 231  
211 His Val Gly Cys Thr Lys Arg Ser Leu Ala Arg Phe Cys  
212 65 70 75  
213  
214  
215 (2) INFORMATION FOR SEQ ID NO:10:  
216  
217 (i) SEQUENCE CHARACTERISTICS:  
218 (A) LENGTH: 593 base pairs  
219 (B) TYPE: nucleic acid  
220 (C) STRANDEDNESS: single  
221 (D) TOPOLOGY: linear  
222  
223 (ii) MOLECULE TYPE: cDNA  
224  
225 (ix) FEATURE:  
226 (A) NAME/KEY: CDS  
227 (B) LOCATION: 431..586  
228  
229 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:  
230  
231 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA 60  
232  
233 GTTGTATTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAA GAACTGTGTG CGCAGGTAGA 120  
234  
235 AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG 180  
236  
237 GTTGATTGAT CAGGTAGAGG GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCTCTGA 240  
238  
239 CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA 300  
240  
241 AAAAGTTAAT CTTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT ATAGTCGCTT 360  
242  
243 TGTTTTTTATT TTTTAATGTA TTTGTACGCA AGTTCACGTA AAAAGGGTAT CTAGAGGTTG 420  
244  
245 AGGTGATTTT ATG AAA AAG AAT ATC GCA TTT CTT CTT GCA TCT ATG TTC 469  
246 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe  
247 1 5 10  
248  
249 GTT TTT TCT ATT GCT ACA AAT GCC TAT GCA GAC TCA TGG ATG GAG GAA 517  
250 Val Phe Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ser Trp Met Glu Glu  
251 15 20 25  
252  
253 GTT ATT AAA TTA TGC GGC CGC GAA TTG GTA CGC GCG CAA ATA GCG ATA 565  
254 Val Ile Lys Leu Cys Gly Arg Glu Leu Val Arg Ala Gln Ile Ala Ile  
255 30 35 40 45

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256
257 TGC GGT ATG AGT ACA TGG AGT TGAAGAA      593
258 Cys Gly Met Ser Thr Trp Ser
259              50
260
261
262 (2) INFORMATION FOR SEQ ID NO:11:
263
264 (i) SEQUENCE CHARACTERISTICS:
265 (A) LENGTH: 1500 base pairs
266 (B) TYPE: nucleic acid
267 (C) STRANDEDNESS: single
268 (D) TOPOLOGY: linear
269
270 (ii) MOLECULE TYPE: cDNA
271
272 (ix) FEATURE:
273 (A) NAME/KEY: CDS
274 (B) LOCATION: 438..1238
275
276 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
277
278 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA      60
279
280 GTTGTATTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAA GAACTGTGTG CGCAGGTAGA      120
281
282 AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG      180
283
284 GTTGATTCAT CAGGTAGAGG GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCTCTGA      240
285
286 CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCTAGTA      300
287
288 AAAAGTTAAT CTTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT ATAGTCGCTT      360
289
290 TGTTTTTTATT TTTTAATGTA TTTGTAACTA GTACGCAAGT TCACGTAAAA AGGGTATCTA      420
291
292 GAGGTTGAGG TGATTTT ATG AAA AAG AAT ATC GCA TTT CTT CTT GCA TCT      470
293 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser
294              1              5              10
295
296 ATG TTC GTT TTT TCT ATT GCT ACA AAT GCC TAT GCA TCA GGC ACT ACA      518
297 Met Phe Val Phe Ser Ile Ala Thr Asn Ala Tyr Ala Ser Gly Thr Thr
298              15              20              25
299
300 AAT ACT GTG GCA GCA TAT AAT TTA ACT TGG AAA TCA ACT AAT TTC AAG      566
301 Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser Thr Asn Phe Lys
302              30              35              40
303
304 ACA ATT TTG GAG TGG GAA CCC AAA CCC GTC AAT CAA GTC TAC ACT GTT      614
305 Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln Val Tyr Thr Val
306              45              50              55

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307																	
308	CAA	ATA	AGC	ACT	AAG	TCA	GGA	GAT	TGG	AAA	AGC	AAA	TGC	TTT	TAC	ACA	662
309	Gln	Ile	Ser	Thr	Lys	Ser	Gly	Asp	Trp	Lys	Ser	Lys	Cys	Phe	Tyr	Thr	
310	60					65						70				75	
311																	
312	ACA	GAC	ACA	GAG	TGT	GAC	CTC	ACC	GAC	GAG	ATT	GTG	AAG	GAT	GTG	AAG	710
313	Thr	Asp	Thr	Glu	Cys	Asp	Leu	Thr	Asp	Glu	Ile	Val	Lys	Asp	Val	Lys	
314					80					85					90		
315																	
316	CAG	ACG	TAC	TTG	GCA	CGG	GTC	TTC	TCC	TAC	CCG	GCA	GGG	AAT	GTG	GAG	758
317	Gln	Thr	Tyr	Leu	Ala	Arg	Val	Phe	Ser	Tyr	Pro	Ala	Gly	Asn	Val	Glu	
318				95					100					105			
319																	
320	AGC	ACC	GGT	TCT	GCT	GGG	GAG	CCT	CTG	TAT	GAG	AAC	TCC	CCA	GAG	TTC	806
321	Ser	Thr	Gly	Ser	Ala	Gly	Glu	Pro	Leu	Tyr	Glu	Asn	Ser	Pro	Glu	Phe	
322			110					115					120				
323																	
324	ACA	CCT	TAC	CTG	GAG	ACA	AAC	CTC	GGA	CAG	CCA	ACA	ATT	CAG	AGT	TTT	854
325	Thr	Pro	Tyr	Leu	Glu	Thr	Asn	Leu	Gly	Gln	Pro	Thr	Ile	Gln	Ser	Phe	
326		125					130					135					
327																	
328	GAA	CAG	GTG	GGA	ACA	AAA	GTG	AAT	GTG	ACC	GTA	GAA	GAT	GAA	CGG	ACT	902
329	Glu	Gln	Val	Gly	Thr	Lys	Val	Asn	Val	Thr	Val	Glu	Asp	Glu	Arg	Thr	
330	140					145					150					155	
331																	
332	TTA	GTC	AGA	AGG	AAC	AAC	ACT	TTC	CTA	AGC	CTC	CGG	GAT	GTT	TTT	GGC	950
333	Leu	Val	Arg	Arg	Asn	Asn	Thr	Phe	Leu	Ser	Leu	Arg	Asp	Val	Phe	Gly	
334					160					165					170		
335																	
336	AAG	GAC	TTA	ATT	TAT	ACA	CTT	TAT	TAT	TGG	AAA	TCT	TCA	AGT	TCA	GGA	998
337	Lys	Asp	Leu	Ile	Tyr	Thr	Leu	Tyr	Tyr	Trp	Lys	Ser	Ser	Ser	Ser	Gly	
338				175					180					185			
339																	
340	AAG	AAA	ACA	GCC	AAA	ACA	AAC	ACT	AAT	GAG	TTT	TTG	ATT	GAT	GTG	GAT	1046
341	Lys	Lys	Thr	Ala	Lys	Thr	Asn	Thr	Asn	Glu	Phe	Leu	Ile	Asp	Val	Asp	
342			190					195					200				
343																	
344	AAA	GGA	GAA	AAC	TAC	TGT	TTC	AGT	GTT	CAA	GCA	GTG	ATT	CCC	TCC	CGA	1094
345	Lys	Gly	Glu	Asn	Tyr	Cys	Phe	Ser	Val	Gln	Ala	Val	Ile	Pro	Ser	Arg	
346		205					210					215					
347																	
348	ACA	GTT	AAC	CGG	AAG	AGT	ACA	GAC	AGC	CCG	GTA	GAG	TGT	ATG	GGC	CAG	1142
349	Thr	Val	Asn	Arg	Lys	Ser	Thr	Asp	Ser	Pro	Val	Glu	Cys	Met	Gly	Gln	
350	220					225					230					235	
351																	
352	GAG	AAA	GGC	CAA	TTC	AGA	GAA	ATA	TTC	TAC	ATC	ATT	GGA	GCT	GTG	GTA	1190
353	Glu	Lys	Gly	Gln	Phe	Arg	Glu	Ile	Phe	Tyr	Ile	Ile	Gly	Ala	Val	Val	
354					240					245					250		
355																	
356	TTT	GTG	GTC	ATC	ATC	CTT	GTC	ATC	ATC	CTG	GCT	ATA	TCT	CTA	CAC	TAAAATTCTC	1245
357	Phe	Val	Val	Ile	Ile	Leu	Val	Ile	Ile	Leu	Ala	Ile	Ser	Leu	His		

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	255	260	265	
358				
359				
360	ATGTTTGACA	GCTTATCATC	GATAAGCTTT	AATGCGGTAG TTTATCACAG TTAAATTGCT 1305
361				
362	AACGCAGTCA	GGCACCGTGT	ATGAAATCTA	ACAATGCGCT CATCGTCATC CTCGGCACCG 1365
363				
364	TCACCCTGGA	TGCTGTAGGC	ATAGGCTTGG	TTATGCCGGT ACTGCCGGGC CTCTTGCGGG 1425
365				
366	ATATCGTCCA	TTCCGACAGC	ATCGCCAGTC	ACTATGGCGT GCTCCTAGCG CTATATGCGT 1485
367				
368	TGATGCAATT	TCTAT		1500
369				
370				

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Arg	Lys
1				5					10	

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Arg	Arg
1				5					10	

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single



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409 (D) TOPOLOGY: linear  
410  
411 (ii) MOLECULE TYPE: peptide  
412  
413 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:  
414  
415 Met Lys Lys Asn Ile Ala Phe Leu Leu Lys Lys  
416 1 5 10  
417  
418  
419 (2) INFORMATION FOR SEQ ID NO:15:  
420  
421 (i) SEQUENCE CHARACTERISTICS:  
422 (A) LENGTH: 42 base pairs  
423 (B) TYPE: nucleic acid  
424 (C) STRANDEDNESS: both  
425 (D) TOPOLOGY: linear  
426  
427 (ii) MOLECULE TYPE: cDNA  
428  
429 (ix) FEATURE:  
430 (A) NAME/KEY: misc\_feature  
431 (B) LOCATION: 5..42  
432 (D) OTHER INFORMATION: /note= "Complementary  
433 double-stranded binding between bases 5 and 42 to  
434 SEQ ID NO:16. "  
435  
436 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:  
437  
438 CTAGAATTAT GAAAAAGAAT ATCGCATTTT TTCTTAAACG GG 42  
439  
440  
441 (2) INFORMATION FOR SEQ ID NO:16:  
442  
443 (i) SEQUENCE CHARACTERISTICS:  
444 (A) LENGTH: 41 base pairs  
445 (B) TYPE: nucleic acid  
446 (C) STRANDEDNESS: both  
447 (D) TOPOLOGY: linear  
448  
449 (ii) MOLECULE TYPE: cDNA  
450  
451 (ix) FEATURE:  
452 (A) NAME/KEY: misc\_feature  
453 (B) LOCATION: 4..41  
454 (D) OTHER INFORMATION: /note= "Complementary  
455 double-stranded binding between bases 4 and 41 to  
456 SEQ ID NO:15. "  
457  
458 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:  
459

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460 AGTCCCGTTT AAGAAGAAAT GCGATATTCT TTTTCATAAT T 41  
461  
462  
463 (2) INFORMATION FOR SEQ ID NO:17:  
464  
465 (i) SEQUENCE CHARACTERISTICS:  
466 (A) LENGTH: 42 base pairs  
467 (B) TYPE: nucleic acid  
468 (C) STRANDEDNESS: both  
469 (D) TOPOLOGY: linear  
470  
471 (ii) MOLECULE TYPE: cDNA  
472  
473 (ix) FEATURE:  
474 (A) NAME/KEY: misc\_feature  
475 (B) LOCATION: 5..42  
476 (D) OTHER INFORMATION: /note= "Complementary  
477 double-stranded binding between bases 5 and 42 to  
478 SEQ ID NO:18."  
479  
480 (ix) FEATURE:  
481 (A) NAME/KEY: CDS  
482 (B) LOCATION: 9..41  
483  
484 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:  
485  
486 CTAGAATT ATG TTC CCA GCT ATG CCT CTA TCT AGT AAA CGG G 42  
487 Met Phe Pro Ala Met Pro Leu Ser Ser Lys Arg  
488 1 5 10  
489  
490  
491 (2) INFORMATION FOR SEQ ID NO:18:  
492  
493 (i) SEQUENCE CHARACTERISTICS:  
494 (A) LENGTH: 41 base pairs  
495 (B) TYPE: nucleic acid  
496 (C) STRANDEDNESS: both  
497 (D) TOPOLOGY: linear  
498  
499 (ii) MOLECULE TYPE: cDNA  
500  
501 (ix) FEATURE:  
502 (A) NAME/KEY: misc\_feature  
503 (B) LOCATION: 4..41  
504 (D) OTHER INFORMATION: /note= "Complementary  
505 double-stranded binding between bases 4 and 41 to  
506 SEQ ID NO:17."  
507  
508 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:  
509  
510 AGTCCCGTTT ACTAGATAGA GGCATAGCTG GGAACATAAT T 41

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511  
512  
513 (2) INFORMATION FOR SEQ ID NO:19:  
514  
515 (i) SEQUENCE CHARACTERISTICS:  
516 (A) LENGTH: 11 amino acids  
517 (B) TYPE: amino acid  
518 (D) TOPOLOGY: linear  
519  
520 (ii) MOLECULE TYPE: protein  
521  
522 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:  
523  
524 Met Phe Pro Ala Met Pro Leu Ser Ser Lys Arg  
525 1 5 10  
526  
527  
528 (2) INFORMATION FOR SEQ ID NO:20:  
529  
530 (i) SEQUENCE CHARACTERISTICS:  
531 (A) LENGTH: 64 base pairs  
532 (B) TYPE: nucleic acid  
533 (C) STRANDEDNESS: both  
534 (D) TOPOLOGY: linear  
535  
536 (ii) MOLECULE TYPE: cDNA  
537  
538 (ix) FEATURE:  
539 (A) NAME/KEY: CDS  
540 (B) LOCATION: 5..64  
541  
542 (ix) FEATURE:  
543 (A) NAME/KEY: misc\_feature  
544 (B) LOCATION: 5..64  
545 (D) OTHER INFORMATION: /note= "Complementary  
546 double-stranded binding between bases 5 and 64 to  
547 SEQ ID NO:21."  
548  
549 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:  
550  
551 CGCG CAG ATT GCC ATT TGC GGC ATG AGC ACC TGG AGC AAA AGG AAA CCC 49  
552 Gln Ile Ala Ile Cys Gly Met Ser Thr Trp Ser Lys Arg Lys Pro  
553 1 5 10 15  
554  
555 ACT GGT TAT GGT TCT 64  
556 Thr Gly Tyr Gly Ser  
557 20  
558  
559  
560 (2) INFORMATION FOR SEQ ID NO:21:  
561

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562 (i) SEQUENCE CHARACTERISTICS:  
563 (A) LENGTH: 62 base pairs  
564 (B) TYPE: nucleic acid  
565 (C) STRANDEDNESS: both  
566 (D) TOPOLOGY: linear  
567  
568 (ii) MOLECULE TYPE: cDNA  
569  
570 (ix) FEATURE:  
571 (A) NAME/KEY: misc\_feature  
572 (B) LOCATION: 3..62  
573 (D) OTHER INFORMATION: /note= "Complementary  
574 double-stranded binding between bases 3 and 62 to  
575 SEQ ID NO:20."  
576  
577 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:  
578  
579 CGAGAACCAT AACCAGTGGG TTTCTTTTGT CTCCAGGTGC TCATGCCGCA AATGGCAATC 60  
580  
581 TG 62  
582  
583  
584 (2) INFORMATION FOR SEQ ID NO:22:  
585  
586 (i) SEQUENCE CHARACTERISTICS:  
587 (A) LENGTH: 20 amino acids  
588 (B) TYPE: amino acid  
589 (D) TOPOLOGY: linear  
590  
591 (ii) MOLECULE TYPE: protein  
592  
593 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:  
594  
595 Gln Ile Ala Ile Cys Gly Met Ser Thr Trp Ser Lys Arg Lys Pro Thr  
596 1 5 10 15  
597  
598 Gly Tyr Gly Ser  
599 20  
600  
601  
602 (2) INFORMATION FOR SEQ ID NO:23:  
603  
604 (i) SEQUENCE CHARACTERISTICS:  
605 (A) LENGTH: 50 base pairs  
606 (B) TYPE: nucleic acid  
607 (C) STRANDEDNESS: both  
608 (D) TOPOLOGY: linear  
609  
610 (ii) MOLECULE TYPE: cDNA  
611  
612 (ix) FEATURE:

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/080,354ADATE: 02/01/94  
TIME: 18:40:04

INPUT SET: S7245.raw

613 (A) NAME/KEY: misc\_feature  
614 (B) LOCATION: 5..50  
615 (D) OTHER INFORMATION: /note= "Complementary  
616 double-stranded binding between bases 5 and 50  
617 with SEQ ID NO:24."  
618  
619 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:  
620  
621 GGCCACTCTG TGCGGTGCTG AACTGGTTGA CGCTCTGCAG TTTGTTTGCG 50  
622  
623  
624 (2) INFORMATION FOR SEQ ID NO:24:  
625  
626 (i) SEQUENCE CHARACTERISTICS:  
627 (A) LENGTH: 50 base pairs  
628 (B) TYPE: nucleic acid  
629 (C) STRANDEDNESS: both  
630 (D) TOPOLOGY: linear  
631  
632 (ii) MOLECULE TYPE: cDNA  
633  
634 (ix) FEATURE:  
635 (A) NAME/KEY: misc\_feature  
636 (B) LOCATION: 6..50  
637 (D) OTHER INFORMATION: /note= "Complementary  
638 double-stranded binding between bases 6 and 50  
639 with SEQ ID NO:23."  
640  
641 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:  
642  
643 GTCACCGCAA ACAAACTGCA GAGCGTCAAC CAGTTCAGCA CCGCAAGAGT 50  
644  
645  
646 (2) INFORMATION FOR SEQ ID NO:25:  
647  
648 (i) SEQUENCE CHARACTERISTICS:  
649 (A) LENGTH: 55 base pairs  
650 (B) TYPE: nucleic acid  
651 (C) STRANDEDNESS: both  
652 (D) TOPOLOGY: linear  
653  
654 (ii) MOLECULE TYPE: cDNA  
655  
656 (ix) FEATURE:  
657 (A) NAME/KEY: misc\_feature  
658 (B) LOCATION: 1..55  
659 (D) OTHER INFORMATION: /note= "Complementary  
660 double-stranded binding between bases 1 and 55  
661 with SEQ ID NO:26."  
662  
663 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/080,354ADATE: 02/01/94  
TIME: 18:40:10

INPUT SET: S7245.raw

664  
665 GGTCCCGAAA CTCTGTGCGG TGCTGAACTG GTTGACGCTC TGCAGTTTGT TTGCG 55  
666  
667  
668 (2) INFORMATION FOR SEQ ID NO:26:  
669  
670 (i) SEQUENCE CHARACTERISTICS:  
671 (A) LENGTH: 64 base pairs  
672 (B) TYPE: nucleic acid  
673 (C) STRANDEDNESS: both  
674 (D) TOPOLOGY: linear  
675  
676 (ii) MOLECULE TYPE: cDNA  
677  
678 (ix) FEATURE:  
679 (A) NAME/KEY: misc\_feature  
680 (B) LOCATION: 6..64  
681 (D) OTHER INFORMATION: /note= "Complementary  
682 double-stranded binding between bases 6 and 64  
683 with SEQ ID NO:25."  
684  
685 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:  
686  
687 GTCACCGCAA ACAAACTGCA GAGCGTCAAC CAGTTCAGCA CCGCACAGAG TTTCGGGACC 60  
688  
689 TGCA 64  
690  
691  
692 (2) INFORMATION FOR SEQ ID NO:27:  
693  
694 (i) SEQUENCE CHARACTERISTICS:  
695 (A) LENGTH: 84 base pairs  
696 (B) TYPE: nucleic acid  
697 (C) STRANDEDNESS: both  
698 (D) TOPOLOGY: linear  
699  
700 (ii) MOLECULE TYPE: cDNA  
701  
702 (ix) FEATURE:  
703 (A) NAME/KEY: misc\_feature  
704 (B) LOCATION: 5..84  
705 (D) OTHER INFORMATION: /note= "Complementary  
706 double-stranded binding between bases 5 and 84  
707 with SEQ ID NO:28."  
708  
709 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:  
710  
711 CTAGAATTAT GATGATTACT CTGCGCAAAC TTCCTCTGGC GGTTCGCGTC GCAGCGGGCG 60  
712  
713 TAATGTCTGC TCAGGCCATG GCCA 84  
714

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/080,354ADATE: 02/01/94  
TIME: 18:40:17

INPUT SET: S7245.raw

715  
716 (2) INFORMATION FOR SEQ ID NO:28:  
717  
718 (i) SEQUENCE CHARACTERISTICS:  
719 (A) LENGTH: 84 base pairs  
720 (B) TYPE: nucleic acid  
721 (C) STRANDEDNESS: both  
722 (D) TOPOLOGY: linear  
723  
724 (ii) MOLECULE TYPE: cDNA  
725  
726 (ix) FEATURE:  
727 (A) NAME/KEY: misc\_feature  
728 (B) LOCATION: 5..84  
729 (D) OTHER INFORMATION: /note= "Complementary  
730 double-stranded binding between bases 5 and 84  
731 with SEQ ID NO:27."  
732  
733 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:  
734  
735 GATCTGGCCA TGGCCTGAGC AGACATTACG CCCGCTGCGA CGGCAACCGC CAGAGGAAGT 60  
736  
737 TTGCGCAGAG TAATCATCAT AATT 84  
738  
739  
740 (2) INFORMATION FOR SEQ ID NO:29:  
741  
742 (i) SEQUENCE CHARACTERISTICS:  
743 (A) LENGTH: 52 base pairs  
744 (B) TYPE: nucleic acid  
745 (C) STRANDEDNESS: both  
746 (D) TOPOLOGY: linear  
747  
748 (ii) MOLECULE TYPE: cDNA  
749  
750 (ix) FEATURE:  
751 (A) NAME/KEY: misc\_feature  
752 (B) LOCATION: 1..52  
753 (D) OTHER INFORMATION: /note= "Complementary  
754 double-stranded binding between bases 1 and 52  
755 with SEQ ID NO:30."  
756  
757 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:  
758  
759 CAACTCTACA GTGCATTGGC TAATAAATGT TGCCATGTTG GTTGTACCAA AA 52  
760  
761  
762 (2) INFORMATION FOR SEQ ID NO:30:  
763  
764 (i) SEQUENCE CHARACTERISTICS:  
765 (A) LENGTH: 60 base pairs

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/080,354ADATE: 02/01/94  
TIME: 18:40:23

INPUT SET: S7245.raw

766 (B) TYPE: nucleic acid  
767 (C) STRANDEDNESS: both  
768 (D) TOPOLOGY: linear  
769  
770 (ii) MOLECULE TYPE: cDNA  
771  
772 (ix) FEATURE:  
773 (A) NAME/KEY: misc\_feature  
774 (B) LOCATION: 5..56  
775 (D) OTHER INFORMATION: /note= "Complementary  
776 double-stranded binding between bases 5 and 56  
777 with SEQ ID NO:29."  
778  
779 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:  
780  
781 GATCTTTTGG TACAACCAAC ATGGCAACAT TTATTAGCCA ATGCACTGTA GAGTTGTGCA 60  
782  
783  
784 (2) INFORMATION FOR SEQ ID NO:31:  
785  
786 (i) SEQUENCE CHARACTERISTICS:  
787 (A) LENGTH: 13 amino acids  
788 (B) TYPE: amino acid  
789 (C) STRANDEDNESS: single  
790 (D) TOPOLOGY: linear  
791  
792 (ii) MOLECULE TYPE: peptide  
793  
794 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:  
795  
796 Asp Lys Lys Arg Thr Gly Tyr Gly Ser Arg Arg Arg Lys  
797 1 5 10  
798  
799  
800 (2) INFORMATION FOR SEQ ID NO:32:  
801  
802 (i) SEQUENCE CHARACTERISTICS:  
803 (A) LENGTH: 13 amino acids  
804 (B) TYPE: amino acid  
805 (C) STRANDEDNESS: single  
806 (D) TOPOLOGY: linear  
807  
808 (ii) MOLECULE TYPE: peptide  
809  
810 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:  
811  
812 Asp Lys Lys Arg Thr Gly Tyr Gly Ser Arg Lys Lys Arg  
813 1 5 10  
814  
815  
816 (2) INFORMATION FOR SEQ ID NO:33:



RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/080,354ADATE: 02/01/94  
TIME: 18:40:29

INPUT SET: S7245.raw

817  
818 (i) SEQUENCE CHARACTERISTICS:  
819 (A) LENGTH: 13 amino acids  
820 (B) TYPE: amino acid  
821 (C) STRANDEDNESS: single  
822 (D) TOPOLOGY: linear  
823  
824 (ii) MOLECULE TYPE: peptide  
825  
826 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:  
827  
828 Lys Arg Lys Pro Thr Gly Tyr Gly Ser Arg Arg Arg Lys  
829 1 5 10  
830  
831

## (2) INFORMATION FOR SEQ ID NO:34:

832  
833  
834 (i) SEQUENCE CHARACTERISTICS:  
835 (A) LENGTH: 77 amino acids  
836 (B) TYPE: amino acid  
--> 837 (D) TOPOLOGY: protein This is not a valid response -  
838 Use "circular", "linear", "both",  
839 (ii) MOLECULE TYPE: protein "unknown"  
--> 841 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34: "unknown"  
842  
843 Met Lys Lys Asn Ile Ala Phe Leu Leu Lys Arg Asp Ser Trp Met Glu  
844 1 5 10 15  
845  
846 Glu Val Ile Lys Leu Cys Gly Arg Glu Leu Val Arg Ala Gln Ile Ala  
847 20 25 30  
848  
849 Ile Cys Gly Met Ser Thr Trp Ser Lys Arg Lys Pro Thr Gly Tyr Gly  
850 35 40 45  
851  
852 Ser Arg Lys Lys Arg Gln Leu Tyr Ser Ala Leu Ala Asn Lys Cys Cys  
853 50 55 60  
854  
855 His Val Gly Cys Thr Lys Arg Ser Leu Ala Arg Phe Cys  
856 65 70 75  
857

## (2) INFORMATION FOR SEQ ID NO:35:

858  
859  
860  
861 (i) SEQUENCE CHARACTERISTICS:  
862 (A) LENGTH: 915 base pairs  
863 (B) TYPE: nucleic acid  
864 (C) STRANDEDNESS: single  
865 (D) TOPOLOGY: linear  
866  
867 (ii) MOLECULE TYPE: cDNA

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/080,354A

DATE: 02/01/94  
TIME: 18:40:36

INPUT SET: S7245.raw

```

868
869      (ix) FEATURE:
870          (A) NAME/KEY: CDS
871          (B) LOCATION: 3..452
872
873      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:
874
875      GC GGC CGC GAA TTA GTT CGC GCG CAG ATT GCC ATT TGC GGC ATG AGC      47
876      Gly Arg Glu Leu Val Arg Ala Gln Ile Ala Ile Cys Gly Met Ser
877          1              5              10              15
878
879      ACC TGG AGC AAA AGG TCT CTG AGC CAG GAA GAT GCT CCT CAG ACA CCT      95
880      Thr Trp Ser Lys Arg Ser Leu Ser Gln Glu Asp Ala Pro Gln Thr Pro
881          20              25              30
882
883      AGA CCA GTG GCA GAA ATT GTG CCA TCC TTC ATC AAC AAA GAT ACA GAA      143
884      Arg Pro Val Ala Glu Ile Val Pro Ser Phe Ile Asn Lys Asp Thr Glu
885          35              40              45
886
887      ACC ATA AAT ATG ATG TCA GAA TTT GTT GCT AAT TTG CCA CAG GAG CTG      191
888      Thr Ile Asn Met Met Ser Glu Phe Val Ala Asn Leu Pro Gln Glu Leu
889          50              55              60
890
891      AAG TTA ACC CTG TCT GAG ATG CAG CCA GCA TTA CCA CAG CTA CAA CAA      239
892      Lys Leu Thr Leu Ser Glu Met Gln Pro Ala Leu Pro Gln Leu Gln Gln
893          65              70              75
894
895      CAT GTA CCT GTA TTA AAA GAT TCC AGT CTT CTC TTT GAA GAA TTT AAG      287
896      His Val Pro Val Leu Lys Asp Ser Ser Leu Leu Phe Glu Glu Phe Lys
897          80              85              90              95
898
899      AAA CTT ATT CGC AAT AGA CAA AGT GAA GCC GCA GAC AGC AGT CCT TCA      335
900      Lys Leu Ile Arg Asn Arg Gln Ser Glu Ala Ala Asp Ser Ser Pro Ser
901          100              105              110
902
903      GAA TTA AAA TAC TTA GGC TTG GAT ACT CAT TCT CGA AAA AAG AGA CAA      383
904      Glu Leu Lys Tyr Leu Gly Leu Asp Thr His Ser Arg Lys Lys Arg Gln
905          115              120              125
906
907      CTC TAC AGT GCA TTG GCT AAT AAA TGT TGC CAT GTT GGT TGT ACC AAA      431
908      Leu Tyr Ser Ala Leu Ala Asn Lys Cys Cys His Val Gly Cys Thr Lys
909          130              135              140
910
911      AGA TCT CTT GCT AGA TTT TGC TGAGATGAAG CTAATTGTGC ACATCTCGTA      482
912      Arg Ser Leu Ala Arg Phe Cys
913          145              150
914
915      TAATATTAC ACATATTCTT AATGACATTT CACTGATGCT TCTATCAGGT CAATTCTCAT      542
916
917      GTTTGACAGC TTATCATCGA TAAGCTTTAA TCGGGTAGTT TATCACAGTT AAATTGCTAA      602
918

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# RAW SEQUENCE LISTING PATENT APPLICATION US/08/080,354A

DATE: 02/01/94  
TIME: 18:40:42

INPUT SET: S7245.raw

```

919 CGCAGTCAGG CACCGTGTAT GAAATCTAAC AATGCGCTCA TCGTCATCCT CGGCACCGTC      662
920
921 ACCCTGGATG CTGTAGGCAT AGGCTTGTTT ATGCCGGTAC TGCCGGGCCT CTTGCGGGAT      722
922
923 ATCGTCCATT CCGACAGCAT CGCCAGTCAC TATGGCGTGC TGCTAGCGCT ATATGCGTTG      782
924
925 ATGCAATTTT TATGCGCACC CGTTCTCGGA GCACTGTCCG ACCGCTTTGG CCGCCGCCCA      842
926
927 GTCCTGCTCG CTTGCTACT TGGAGCCACT ATCGACTACG CGATCATGGC GACCACACCC      902
928
929 GTCCTGTGGA TCC      915
930
931
932 (2) INFORMATION FOR SEQ ID NO:36:
933
934     (i) SEQUENCE CHARACTERISTICS:
935         (A) LENGTH: 150 amino acids
936         (B) TYPE: amino acid
937         (D) TOPOLOGY: linear
938
939     (ii) MOLECULE TYPE: protein
940
941     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:
942
943 Gly Arg Glu Leu Val Arg Ala Gln Ile Ala Ile Cys Gly Met Ser Thr
944   1             5             10             15
945
946 Trp Ser Lys Arg Ser Leu Ser Gln Glu Asp Ala Pro Gln Thr Pro Arg
947             20             25             30
948
949 Pro Val Ala Glu Ile Val Pro Ser Phe Ile Asn Lys Asp Thr Glu Thr
950             35             40             45
951
952 Ile Asn Met Met Ser Glu Phe Val Ala Asn Leu Pro Gln Glu Leu Lys
953             50             55             60
954
955 Leu Thr Leu Ser Glu Met Gln Pro Ala Leu Pro Gln Leu Gln Gln His
956             65             70             75             80
957
958 Val Pro Val Leu Lys Asp Ser Ser Leu Leu Phe Glu Glu Phe Lys Lys
959             85             90             95
960
961 Leu Ile Arg Asn Arg Gln Ser Glu Ala Ala Asp Ser Ser Pro Ser Glu
962             100            105            110
963
964 Leu Lys Tyr Leu Gly Leu Asp Thr His Ser Arg Lys Lys Arg Gln Leu
965             115            120            125
966
967 Tyr Ser Ala Leu Ala Asn Lys Cys Cys His Val Gly Cys Thr Lys Arg
968             130            135            140
969

```

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/080,354ADATE: 02/01/94  
TIME: 18:40:49

INPUT SET: S7245.raw

970 Ser Leu Ala Arg Phe Cys  
971 145 150  
972  
973  
974 (2) INFORMATION FOR SEQ ID NO:37:  
975  
976 (i) SEQUENCE CHARACTERISTICS:  
977 (A) LENGTH: 52 amino acids  
978 (B) TYPE: amino acid  
979 (D) TOPOLOGY: linear  
980  
981 (ii) MOLECULE TYPE: protein  
982  
983 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:  
984  
985 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser  
986 1 5 10 15  
987  
988 Ile Ala Thr Asn Ala Tyr Ala Asp Ser Trp Met Glu Glu Val Ile Lys  
989 20 25 30  
990  
991 Leu Cys Gly Arg Glu Leu Val Arg Ala Gln Ile Ala Ile Cys Gly Met  
992 35 40 45  
993  
994 Ser Thr Trp Ser  
995 50  
996  
997  
998 (2) INFORMATION FOR SEQ ID NO:38:  
999  
1000 (i) SEQUENCE CHARACTERISTICS:  
1001 (A) LENGTH: 266 amino acids  
1002 (B) TYPE: amino acid  
1003 (D) TOPOLOGY: linear  
1004  
1005 (ii) MOLECULE TYPE: protein  
1006  
1007 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:  
1008  
1009 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser  
1010 1 5 10 15  
1011  
1012 Ile Ala Thr Asn Ala Tyr Ala Ser Gly Thr Thr Asn Thr Val Ala Ala  
1013 20 25 30  
1014  
1015 Tyr Asn Leu Thr Trp Lys Ser Thr Asn Phe Lys Thr Ile Leu Glu Trp  
1016 35 40 45  
1017  
1018 Glu Pro Lys Pro Val Asn Gln Val Tyr Thr Val Gln Ile Ser Thr Lys  
1019 50 55 60  
1020

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/080,354ADATE: 02/01/94  
TIME: 18:40:55

INPUT SET: S7245.raw

```
1021 Ser Gly Asp Trp Lys Ser Lys Cys Phe Tyr Thr Thr Asp Thr Glu Cys
1022 65 70 75 80
1023
1024 Asp Leu Thr Asp Glu Ile Val Lys Asp Val Lys Gln Thr Tyr Leu Ala
1025 85 90 95
1026
1027 Arg Val Phe Ser Tyr Pro Ala Gly Asn Val Glu Ser Thr Gly Ser Ala
1028 100 105 110
1029
1030 Gly Glu Pro Leu Tyr Glu Asn Ser Pro Glu Phe Thr Pro Tyr Leu Glu
1031 115 120 125
1032
1033 Thr Asn Leu Gly Gln Pro Thr Ile Gln Ser Phe Glu Gln Val Gly Thr
1034 130 135 140
1035
1036 Lys Val Asn Val Thr Val Glu Asp Glu Arg Thr Leu Val Arg Arg Asn
1037 145 150 155 160
1038
1039 Asn Thr Phe Leu Ser Leu Arg Asp Val Phe Gly Lys Asp Leu Ile Tyr
1040 165 170 175
1041
1042 Thr Leu Tyr Tyr Trp Lys Ser Ser Ser Ser Gly Lys Lys Thr Ala Lys
1043 180 185 190
1044
1045 Thr Asn Thr Asn Glu Phe Leu Ile Asp Val Asp Lys Gly Glu Asn Tyr
1046 195 200 205
1047
1048 Cys Phe Ser Val Gln Ala Val Ile Pro Ser Arg Thr Val Asn Arg Lys
1049 210 215 220
1050
1051 Ser Thr Asp Ser Pro Val Glu Cys Met Gly Gln Glu Lys Gly Gln Phe
1052 225 230 235 240
1053
1054 Arg Glu Ile Phe Tyr Ile Ile Gly Ala Val Val Phe Val Val Ile Ile
1055 245 250 255
1056
1057 Leu Val Ile Ile Leu Ala Ile Ser Leu His
1058 260 265
1059
1060
```

## (2) INFORMATION FOR SEQ ID NO:39:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 301 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/080,354A

DATE: 02/01/94  
TIME: 18:41:01

INPUT SET: S7245.raw

```

1072      (A) NAME/KEY: CDS
1073      (B) LOCATION: 7..297
1074
1075      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:
1076
1077      AAGCTT ATG AAA TCT AAC AAT GCG CTC ATC GTC ATC CTC GGC ACC GTC      48
1078      Met Lys Ser Asn Asn Ala Leu Ile Val Ile Leu Gly Thr Val
1079      1          5          10
1080
1081      ACC CTG GAT GCT GTA GGC ATA GGC TTG GTT ATG CCG GTA CTG CCG GGC      96
1082      Thr Leu Asp Ala Val Gly Ile Gly Leu Val Met Pro Val Leu Pro Gly
1083      15          20          25          30
1084
1085      CTC TTG CGG GAT ATC GTC CAT TCC GAC AGC ATC GCC AGT CAC TAT GGC      144
1086      Leu Leu Arg Asp Ile Val His Ser Asp Ser Ile Ala Ser His Tyr Gly
1087      35          40          45
1088
1089      GTG CTG CTA GCG CTA TAT GCG TTG ATG CAA TTT CTA TGC GCA CCC GTT      192
1090      Val Leu Leu Ala Leu Tyr Ala Leu Met Gln Phe Leu Cys Ala Pro Val
1091      50          55          60
1092
1093      CTC GGA GCA CTG TCC GAC CGC TTT GGC CGC CGC CCA GTC CTG CTC GCT      240
1094      Leu Gly Ala Leu Ser Asp Arg Phe Gly Arg Arg Pro Val Leu Leu Ala
1095      65          70          75
1096
1097      TCG CTA CTT GGA GCC ACT ATC GAC TAC GCG ATC ATG GCG ACC ACA CCC      288
1098      Ser Leu Leu Gly Ala Thr Ile Asp Tyr Ala Ile Met Ala Thr Thr Pro
1099      80          85          90
1100
1101      GTC CTG TGG ATCC      301
1102      Val Leu Trp
1103      95
1104
1105
1106      (2) INFORMATION FOR SEQ ID NO:40:
1107
1108      (i) SEQUENCE CHARACTERISTICS:
1109      (A) LENGTH: 97 amino acids
1110      (B) TYPE: amino acid
1111      (D) TOPOLOGY: linear
1112
1113      (ii) MOLECULE TYPE: protein
1114
1115      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:
1116
1117      Met Lys Ser Asn Asn Ala Leu Ile Val Ile Leu Gly Thr Val Thr Leu
1118      1          5          10          15
1119
1120      Asp Ala Val Gly Ile Gly Leu Val Met Pro Val Leu Pro Gly Leu Leu
1121      20          25          30
1122

```

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/080,354ADATE: 02/01/94  
TIME: 18:41:08

INPUT SET: S7245.raw

```
1123 Arg Asp Ile Val His Ser Asp Ser Ile Ala Ser His Tyr Gly Val Leu
1124      35                      40                      45
1125
1126 Leu Ala Leu Tyr Ala Leu Met Gln Phe Leu Cys Ala Pro Val Leu Gly
1127      50                      55                      60
1128
1129 Ala Leu Ser Asp Arg Phe Gly Arg Arg Pro Val Leu Leu Ala Ser Leu
1130      65                      70                      75                      80
1131
1132 Leu Gly Ala Thr Ile Asp Tyr Ala Ile Met Ala Thr Thr Pro Val Leu
1133      85                      90                      95
1134
1135 Trp
1136
1137
1138
```

PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/080,354A**

DATE: 02/01/94  
TIME: 18:41:10

*INPUT SET: S7245.raw*

Line	Error	Original Text
837	Wrong or Missing Sequence Topology	(D) TOPOLOGY: protein
841	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:



PAGE: 1

**SEQUENCE MISSING ITEM REPORT**  
**PATENT APPLICATION US/08/080,354A**

DATE: 02/01/94  
TIME: 18:41:11

*INPUT SET: S7245.raw*

APPLICATION NUMBER  
FILING DATE  
PRIOR APPLICATION DATA

**SEQUENCE CORRECTION REPORT**  
**PATENT APPLICATION US/08/080,354A**

DATE: 02/01/94  
TIME: 18:41:11

*INPUT SET: S7245.raw*

Line	Original Text	Corrected Text
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